

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/781,880
DATE: 03/19/2001
TIME: 13:09:42

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03192001\I781880.raw

ENTERED

4 <110> APPLICANT: Glucksmann, Maria Alexandra
5 Silos-Santiago, Inmaculada
7 <120> TITLE OF INVENTION: Novel Seven-Transmembrane
8 Proteins/G-Protein Coupled Receptors
11 <130> FILE REFERENCE: 35800/208932
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/781,880
C--> 13 <141> CURRENT FILING DATE: 2001-02-12
13 <150> PRIOR APPLICATION NUMBER: 60/182,061
14 <151> PRIOR FILING DATE: 2000-02-11
16 <160> NUMBER OF SEQ ID NOS: 10
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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21 <211> LENGTH: 1875
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (323)...(1522)
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (1)...(1875)
31 <223> OTHER INFORMATION: n = A,T,C or G
33 <400> SEQUENCE: 1
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W--> 35 agtcaagggc agatttgggn tcattgaacn tcacttccaa ggtcaaggat tctcatgctc 120
36 agtttgcaag gagtgagatt acagtggcct gcacctggct tattttgqta ttttaagtaa 180
37 agacagggtt tcacctggtt ggccaggctg ttcttgaact cctgacctca agtgttcccc 240
W--> 38 ntgcctcggt cctcccaaa tgctgggatt acaggcatga accaccatcc ccagccttct 300
39 ctcttcttaa taatggcttt ctatg tct ttc act tct ctc ata ccc tca ctc 352
40 Met Ser Phe Thr Ser Leu Ile Pro Ser Leu
41 1 5 10
43 tgt ttc tcc ttg act ctc cca ttc ctg ttt tgt tat ctt tct tta tgg 400
44 Cys Phe Ser Leu Thr Leu Pro Phe Leu Phe Cys Tyr Leu Ser Leu Trp
45 15 20 25
47 ccg ttt ctt tct gct ttt ctg ttt atc act cgc tgg cta ctt gcc ttt 448
48 Pro Phe Leu Ser Ala Phe Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe
49 30 35 40
51 ctc tct cta ttc tct gtc tct gtc cct gtt tct tct gtt tca agt tca 496
52 Leu Ser Leu Phe Ser Val Ser Val Pro Val Ser Ser Val Ser Ser
53 45 50 55
55 atg gtt ctc tgt ctc tat ctc tct gtt tct gcc tct ccg tct gtc ttt 544
56 Met Val Leu Cys Leu Tyr Leu Ser Val Ser Ala Ser Pro Ser Val Phe
57 60 65 70
59 tgt ttc tct tgc atg cag gcc ccc ata ctg tgg atc atg gca aat ctg 592
60 Cys Phe Ser Cys Met Gln Gly Pro Ile Leu Trp Ile Met Ala Asn Leu
61 75 80 85 90
63 agc cag ccc tcc gaa ttt gtc ctc ttg gcc ttc tcc tcc ttt ggt gag 640
64 Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser Ser Phe Gly Glu

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65	95	100	105	
67 ctg cag gcc ctt ctg tat ggc ccc ttc ctc atg ctt tat ctt ctc gcc				688
68 Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala				
69	110	115	120	
71 ttc atg gga aac acc atc atc ata gtt atg gtc ata gct gac acc cac				736
72 Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp Thr His				
73	125	130	135	
75 cta cat aca ccc atg tac ttc ttc ctg ggc aat ttt tcc ctg ctg gag				784
76 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu				
77	140	145	150	
79 atc ttg gta acc atg act gca gtg ccc agg atg ctc tca gac ctg ttg				832
80 Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu				
81 155	160	165	170	
83 gtc ccc cac aaa gtc att acc ttc act ggc tgc atg gtc cag ttc tac				880
84 Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr				
85	175	180	185	
87 ttc cac ttt tcc ctg qgg tcc acc tcc ttc ctc atc ctg aca gac atg				928
88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met				
89	190	195	200	
91 gcc ctt gat cgc ttt gtg gcc atc tgc cac cca ctg cgc tat gcc act				976
92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr				
93	205	210	215	
95 ctg atg agc cgg gct atg tgt gtc cag ctg gct ggg gct gcc tgg gca				1024
96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala				
97	220	225	230	
99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt				1072
100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu				
101 235	240	245	250	
103 gat tac tgc cat ggc ggc gtc atc aac cac ttc ttc tgt gac aat gaa				1120
104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu				
105	255	260	265	
107 cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gaa ttc tgg				1168
108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp				
109	270	275	280	
111 gac ttt ctg atg gcc ttg acc ttt gtc ctc agc tcc ttc ctg gtg acc				1216
112 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr				
113	285	290	295	
115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct				1264
116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser				
117	300	305	310	
119 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca				1312
120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr				
121 315	320	325	330	
123 ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct				1360
124 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro				
125	335	340	345	
127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act				1408
128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr				
129	350	355	360	

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131 tca gtt ctc acc ccc ttt ctc aat ccc ttt atc ctt acc ttc tgc aat      1456
132 Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn
133      365      370      375
135 cag aca gtt aaa aca gtg cta cag ggg cag atg cag agg ctg aaa ggc      1504
136 Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln Arg Leu Lys Gly
137      380      385      390
139 ctt tgc aag gca caa tga tgaagcccagg gccaggggga acctggcctg      1552
140 Leu Cys Lys Ala Gln *
141 395
143 cctccattga gcagttctgt ggggagggag acctccagca agtgggaaga acactgctga      1612
144 gtttcttttag tttttttccc tctgagcaat aactacagtg agccctgagt gctgcactgt      1672
145 ctggcccaaa gctcttatgg accaccatgg aagagttccc tacatccct ggcagccgta      1732
146 agaactctga gactagccca gacttttcag taaaggggag tgcattgtgt ttgcatttaa      1792
147 ggaagagcag ccmagaagtg ctctatgac aagaggtagt cgacgcggcc gcgtcgacgg      1852
148 aagctgggat acagcattta atg      1875
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 399
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 2
156 Met Ser Phe Thr Ser Leu Ile Pro Ser Leu Cys Phe Ser Leu Thr Leu
157 1 5 10 15
158 Pro Phe Leu Phe Cys Tyr Leu Ser Leu Trp Pro Phe Leu Ser Ala Phe
159 20 25 30
160 Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe Leu Ser Leu Phe Ser Val
161 35 40 45
162 Ser Val Pro Val Ser Ser Val Ser Ser Met Val Leu Cys Leu Tyr
163 50 55 60
164 Leu Ser Val Ser Ala Ser Pro Ser Val Phe Cys Phe Ser Cys Met Gln
165 65 70 75 80
166 Gly Pro Ile Leu Trp Ile Met Ala Asn Leu Ser Gln Pro Ser Glu Phe
167 85 90 95
168 Val Leu Leu Gly Phe Ser Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr
169 100 105 110
170 Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile
171 115 120 125
172 Ile Ile Val Met Val Ile Ala Asp Thr His Leu His Thr Pro Met Tyr
173 130 135 140
174 Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu Ile Leu Val Thr Met Thr
175 145 150 155 160
176 Ala Val Pro Arg Met Leu Ser Asp Leu Leu Val Pro His Lys Val Ile
177 165 170 175
178 Thr Phe Thr Gly Cys Met Val Gln Phe Tyr Phe His Phe Ser Leu Gly
179 180 185 190
180 Ser Thr Ser Phe Leu Ile Leu Thr Asp Met Ala Leu Asp Arg Phe Val
181 195 200 205
182 Ala Ile Cys His Pro Leu Arg Tyr Gly Thr Leu Met Ser Arg Ala Met
183 210 215 220
184 Cys Val Gln Leu Ala Gly Ala Ala Trp Ala Ala Pro Phe Leu Ala Met

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185 225          230          235          240
186 Val Pro Thr Val Leu Ser Arg Ala His Leu Asp Tyr Cys His Gly Gly
187          245          250          255
188 Val Ile Asn His Phe Phe Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser
189          260          265          270
190 Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp Asp Phe Leu Met Ala Leu
191          275          280          285
192 Thr Phe Val Leu Ser Ser Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr
193          290          295          300
194 Ile Val Thr Thr Val Leu Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys
195          305          310          315          320
196 Ala Phe Ser Thr Cys Gly Ser His Leu Thr Leu Val Phe Ile Gly Tyr
197          325          330          335
198 Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro Gly Lys Ala His Ser Val
199          340          345          350
200 Gln Val Arg Lys Val Val Ala Leu Val Thr Ser Val Leu Thr Pro Phe
201          355          360          365
202 Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn Gln Thr Val Lys Thr Val
203          370          375          380
204 Leu Gln Gly Gln Met Gln Arg Leu Lys Gly Leu Cys Lys Ala Gln
205          385          390          395
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208 <211> LENGTH: 1200
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 3
213 atgtctttca ctctctcat accctcactc tgtttctcct tgactctccc attcctgttt      60
214 tgttatcttt ctctatggcc gtttctttct gctttctctt ttatcactcg ctggtacttt      120
215 gcctttctct ctctattctc tgtctctgtc cctgtttctt ctgtttcaag tcaaatggtt      180
216 ctctgtctct atctctctgt ttctgctctt cgtctgtctt ttgtttctc ttgcatgcag      240
217 ggcctccatac tgtggatcat ggcaaatctg agccagccct ccgaatttgt cctcttgggc      300
218 ttctctctct ttggtgagct qcagccctt ctgtatggcc ccttctctat gctttatctt      360
219 ctgccttcca tgggaacac catcatcata gttatggtca tagctgacac ccacctacat      420
220 acacccatgt acttcttctt gggcaatttt tccctgctgg agatcttggg aacctgact      480
221 gcagtgccta ggatgctctc agacctgttg gtccccaca aagtcattac ctctactggc      540
222 tgcattggtcc agttctactt ccacttttcc ctgggggtcca cctccttct catctgaca      600
223 gacatggccc ttgctgctt tgtggccatc tgcacccac tgcctatagg cactctgatg      660
224 agccgggcta tgtgtgtcca gctggctggg gctgcctggg cagctccttt cctagccatg      720
225 gtaccacttg tctctctccc agctcatctt gattactgcc atggcggcgt catcaaccac      780
226 ttcttctgtg acaatgaacc tctcctgcag ttgtcatgct ctgacactcg cctgttgaa      840
227 ttctgggact ttctgatggc cttgaccttt gtctcagct ccttcttggg gacctcaco      900
228 tctataggct acatagtgc cactgtgctg cggatccctt ctgccagcag ctgccagaag      960
229 gctttctcca cttgcyggtc tcacctcaca ctggtcttca tcggtacag tagtaccatc      1020
230 ttctgtatg tcaggcctgg caaagctcac tctgtgcaag tcaggaaagt cgtggccttg      1080
231 gtgacttcag ttctcaccct ctttctcaat ccttttatcc ttacctctg caatcagaca      1140
232 gttaaaacag tgcacaggg gcagatgcag agcctgaaag gctttgcaa ggcacaatga      1200
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 3630
236 <212> TYPE: DNA

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 TIME: 13:09:42

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\03192001\I781880.raw

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237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (343)...(2334)
243 <400> SEQUENCE: 4
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245 cgcgaagcgc tgctgccgcg qacqatggcg accgtacggg ccgagccgct gccgctgccc 120
246 ctgcctccgc ctccccagaa gcaacatccg aggcctcggc cagaagagcc gccgctgtga 180
247 gccgtgccgt accggccccc gccgcccgcg gaggagaacg ggagggcggg cgagagagcc 240
248 ggggagttgc ggagcccgcg cgcgggcagc gccgctcccc agggagggag tccgcagcct 300
249 gaggtcttct ccaagaaaaa aaaaaagaaa aaaaaaaca ac latg gct qca aag 354
250 Met Ala Ala Lys
251 1
253 gag aaa ctg gag gca gtg tta aat gtg gcc ctg agg gtg cca agc atc 402
254 Glu Lys Leu Glu Ala Val Leu Asn Val Ala Leu Arg Val Pro Ser Ile
255 5 10 15 20
257 atg ctg ttg gat gtc ctg tac aga tgg gat gtc agc tcc ttt ttc cag 450
258 Met Leu Leu Asp Val Leu Tyr Arg Trp Asp Val Ser Ser Phe Phe Gln
259 25 30 35
261 cag atc caa aga agt agc ctt agt aat aac cct ctt ttc cag tat aag 498
262 Gln Ile Gln Arg Ser Ser Leu Ser Asn Asn Pro Leu Phe Glu Tyr Lys
263 40 45 50
265 tat ttg gct ctt aat atg cat tat gta ggt tat atc tta agt gtg gtg 546
266 Tyr Leu Ala Leu Asn Met His Tyr Val Gly Tyr Ile Leu Ser Val Val
267 55 60 65
269 ctg cta aca ttg ccc agg cag cat ctg gtt cag ctt tat cta tat ttt 594
270 Leu Leu Thr Leu Pro Arg Gln His Leu Val Gln Leu Tyr Leu Tyr Phe
271 70 75 80
273 ttg act gct ctg ctc ctc tat gct gga cat caa att tcc agg gac tat 642
274 Leu Thr Ala Leu Leu Tyr Ala Gly His Gln Ile Ser Arg Asp Tyr
275 85 90 95 100
277 gtt cgg agt gaa ctg gag ttt gcc tat gag gga cca atg tat tta gaa 690
278 Val Arg Ser Glu Leu Glu Phe Ala Tyr Glu Gly Pro Met Tyr Leu Glu
279 105 110 115
281 cct ctc tct atg aat cgg ttt acc aca gcc tta ata ggt cag ttg gtg 738
282 Pro Leu Ser Met Asn Arg Phe Thr Thr Ala Leu Ile Gly Gln Leu Val
283 120 125 130
285 gtg tgt act tta tgc tcc tgt gtc atg aaa aca aag cag att tgg ctg 786
286 Val Cys Thr Leu Cys Ser Cys Val Met Lys Thr Lys Gln Ile Trp Leu
287 135 140 145
289 ttt tca gct cac atg ctt cct ctg cta gca cga ctc tgc ctt gtt cct 834
290 Phe Ser Ala His Met Leu Pro Leu Leu Ala Arg Leu Cys Leu Val Pro
291 150 155 160
293 ttg gag aca att gtt atc atc aat aaa ttt gct atg att ttt act gga 882
294 Leu Glu Thr Ile Val Ile Ile Asn Lys Phe Ala Met Ile Phe Thr Gly
295 165 170 175 180
297 ttg gaa gtt ctc tat ttt ctt ggg tct aat ctt ttg gta cct tat aac 930
298 Leu Glu Val Leu Tyr Phe Leu Gly Ser Asn Leu Leu Val Pro Tyr Asn
299 185 190 195

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VERIFICATION SUMMARY DATE: 03/19/2001
PATENT APPLICATION: US/09/781,880 TIME: 13:09:43

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03192001\I781880.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1